

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/955,572DATE: 01/24/98
TIME: 17:34:07

INPUT SET: S22823.raw

#12

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Kwon, Byoung Se
6
7 (ii) TITLE OF INVENTION: New Receptor and Related Products and
8 Methods
9
10 (iii) NUMBER OF SEQUENCES: 8
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Barnard, Brown & Michaels
14 (B) STREET: 306 East State Street, Suite 220
15 (C) CITY: Ithaca
16 (D) STATE: NY
17 (E) COUNTRY: USA
18 (F) ZIP: 14850
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: 08/955,572
28 (B) FILING DATE: 22-OCT-1997
29 (C) CLASSIFICATION: 435
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: 08/461,652
33 (B) FILING DATE:
34
35 (A) APPLICATION NUMBER: US 08/122,796
36 (B) FILING DATE: 13-SEP-1993
37
38 (vii) PRIOR APPLICATION DATA:
39 (A) APPLICATION NUMBER: US 08/012,269
40 (B) FILING DATE: 01-FEB-1993
41
42 (vii) PRIOR APPLICATION DATA:
43 (A) APPLICATION NUMBER: US 07/922,996
44 (B) FILING DATE: 30-JUL-1992
45
46 (vii) PRIOR APPLICATION DATA:

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47 (A) APPLICATION NUMBER: US 08/267,577
48 (B) FILING DATE: 07-NOV-1988
49
50 (viii) ATTORNEY/AGENT INFORMATION:
51 (A) NAME: Michaels, Christopher A
52 (B) REGISTRATION NUMBER: 34,390
53 (C) REFERENCE/DOCKET NUMBER: KWO4
54
55 (ix) TELECOMMUNICATION INFORMATION:
56 (A) TELEPHONE: 607-273-1711
57 (B) TELEFAX: 607-273-2609
58
59
60 (2) INFORMATION FOR SEQ ID NO:1:
61
62 (i) SEQUENCE CHARACTERISTICS:
63 (A) LENGTH: 838 base pairs
64 (B) TYPE: nucleic acid
65 (C) STRANDEDNESS: double
66 (D) TOPOLOGY: linear
67
68 (ii) MOLECULE TYPE: cDNA to mRNA
69
70 (iii) HYPOTHETICAL: NO
71
72 (iv) ANTI-SENSE: NO
73
74 (vi) ORIGINAL SOURCE:
75 (A) ORGANISM: Homo sapiens
76 (C) INDIVIDUAL ISOLATE: H4-1BB #1
77 (D) DEVELOPMENTAL STAGE: Differentiated T-cell
78 (G) CELL TYPE: Lymphocyte
79
80 (ix) FEATURE:
81 (A) NAME/KEY: CDS
82 (B) LOCATION: 41..805
83 (D) OTHER INFORMATION: /codon_start= 41
84 /product= "H4-1BB"
85 /number= 1
86
87 (ix) FEATURE:
88 (A) NAME/KEY: mat_peptide
89 (B) LOCATION: 41..802
90 (D) OTHER INFORMATION: /codon_start= 41
91 /product= "H4-1BB"
92 /number= 1
93
94
95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
96
97 AATCAGCTTT GCTAGTATCA TACCTGTGCC AGATTCATC ATG GGA AAC AGC TGT 55
98 Met Gly Asn Ser Cys
99 1 5

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100																	
101	TAC	AAC	ATA	GTA	GCC	ACT	CTG	TTG	CTG	GTC	CTC	AAC	TTT	GAG	AGG	ACA	103
102	Tyr	Asn	Ile	Val	Ala	Thr	Leu	Leu	Leu	Val	Leu	Asn	Phe	Glu	Arg	Thr	
103					10					15					20		
104																	
105	AGA	TCA	TTG	CAG	GAT	CCT	TGT	AGT	AAC	TGC	CCA	GCT	GGT	ACA	TTC	TGT	151
106	Arg	Ser	Leu	Gln	Asp	Pro	Cys	Ser	Asn	Cys	Pro	Ala	Gly	Thr	Phe	Cys	
107				25					30					35			
108																	
109	GAT	AAT	AAC	AGG	AAT	CAG	ATT	TGC	AGT	CCC	TGT	CCT	CCA	AAT	AGT	TTC	199
110	Asp	Asn	Asn	Arg	Asn	Gln	Ile	Cys	Ser	Pro	Cys	Pro	Pro	Asn	Ser	Phe	
111			40					45					50				
112																	
113	TCC	AGC	GCA	GGT	GGA	CAA	AGG	ACC	TGT	GAC	ATA	TGC	AGG	CAG	TGT	AAA	247
114	Ser	Ser	Ala	Gly	Gly	Gln	Arg	Thr	Cys	Asp	Ile	Cys	Arg	Gln	Cys	Lys	
115		55					60					65					
116																	
117	GGT	GTT	TTC	AGG	ACC	AGG	AAG	GAG	TGT	TCC	TCC	ACC	AGC	AAT	GCA	GAG	295
118	Gly	Val	Phe	Arg	Thr	Arg	Lys	Glu	Cys	Ser	Ser	Thr	Ser	Asn	Ala	Glu	
119	70					75					80					85	
120																	
121	TGT	GAC	TGC	ACT	CCA	GGG	TTT	CAC	TGC	CTG	GGG	GCA	GGA	TGC	AGC	ATG	343
122	Cys	Asp	Cys	Thr	Pro	Gly	Phe	His	Cys	Leu	Gly	Ala	Gly	Cys	Ser	Met	
123					90					95					100		
124																	
125	TGT	GAA	CAG	GAT	TGT	AAA	CAA	GGT	CAA	GAA	CTG	ACA	AAA	AAA	GGT	TGT	391
126	Cys	Glu	Gln	Asp	Cys	Lys	Gln	Gly	Gln	Glu	Leu	Thr	Lys	Lys	Gly	Cys	
127				105					110					115			
128																	
129	AAA	GAC	TGT	TGC	TTT	GGG	ACA	TTT	AAC	GAT	CAG	AAA	CGT	GGC	ATC	TGT	439
130	Lys	Asp	Cys	Cys	Phe	Gly	Thr	Phe	Asn	Asp	Gln	Lys	Arg	Gly	Ile	Cys	
131			120					125					130				
132																	
133	CGA	CCC	TGG	ACA	AAC	TGT	TCT	TTG	GAT	GGA	AAG	TCT	GTG	CTT	GTG	AAT	487
134	Arg	Pro	Trp	Thr	Asn	Cys	Ser	Leu	Asp	Gly	Lys	Ser	Val	Leu	Val	Asn	
135		135					140					145					
136																	
137	GGG	ACG	AAG	GAG	AGG	GAC	GTG	GTC	TGT	GGA	CCA	TCT	CCA	GCT	GAC	CTC	535
138	Gly	Thr	Lys	Glu	Arg	Asp	Val	Val	Cys	Gly	Pro	Ser	Pro	Ala	Asp	Leu	
139	150					155					160						

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153   AAA CGG GGC AGA AAG AAA CTC CTG TAT ATA TTC AAA CAA CCA TTT ATG      727
154   Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
155       215                      220                      225
156
157   AGA CCA GTA CAA ACT ACT CAA GAG GAA GAT GGC TGT AGC TGC CGA TTT      775
158   Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
159   230                      235                      240                      245
160
161   CCA GAA GAA GAA GAA GGA GGA TGT GAA CTG TGAAATGGAA GTCAATAGGG      825
162   Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
163       250                      255
164
165   CTGTTGGGAC TTT      838
166
167
168   (2) INFORMATION FOR SEQ ID NO:2:
169
170       (i) SEQUENCE CHARACTERISTICS:
171           (A) LENGTH: 255 amino acids
172           (B) TYPE: amino acid
173           (D) TOPOLOGY: linear
174
175       (ii) MOLECULE TYPE: protein
176
177       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
178
179   Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
180       1                      5                      10                      15
181
182   Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
183       20                      25                      30
184
185   Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
186       35                      40                      45
187
188   Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
189       50                      55                      60
190
191   Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
192       65                      70                      75                      80
193
194   Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
195       85                      90                      95
196
197   Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
198       100                     105                     110
199
200   Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
201       115                     120                     125
202
203   Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
204       130                     135                     140
205

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206 Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
207 145 150 155 160
208
209 Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
210 165 170 175
211
212 Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
213 180 185 190
214
215 Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
216 195 200 205
217
218 Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
219 210 215 220
220
221 Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
222 225 230 235 240
223
224 Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
225 245 250 255
226

(2) INFORMATION FOR SEQ ID NO:3:

228
229 (i) SEQUENCE CHARACTERISTICS:
230 (A) LENGTH: 20 base pairs
231 (B) TYPE: nucleic acid
232 (C) STRANDEDNESS: single
233 (D) TOPOLOGY: linear
234
235 (ii) MOLECULE TYPE: other nucleic acid
236 (A) DESCRIPTION: /desc = "PCR Primer"
237
238 (iii) HYPOTHETICAL: NO
239
240 (iv) ANTI-SENSE: NO
241
242
243
244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

245
246
247 TTYTGyMGAA ARTAYAAyCC
248

20

(2) INFORMATION FOR SEQ ID NO:4:

250
251 (i) SEQUENCE CHARACTERISTICS:
252 (A) LENGTH: 20 base pairs
253 (B) TYPE: nucleic acid
254 (C) STRANDEDNESS: single
255 (D) TOPOLOGY: linear
256
257 (ii) MOLECULE TYPE: other nucleic acid
258 (A) DESCRIPTION: /desc = "PCR Primer"

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SEQUENCE VERIFICATION REPORT
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Original Text